Amendments to the Specification

In the specification:

Please replace the title with the following amended title:

"Nucleic Acid Encoding a Polypeptide Homologous to a Potassium Channel Protein."

Please replace the paragraph bridging pages 11-12 with the following amended paragraph:

The Expect value is used as a convenient way to create a significance threshold for reporting results. The default value used for blasting is typically set to 0.0001. In BLAST 2.0, the Expect value is also used instead of the P value (probability) to report the significance of matches. For example, an E value of one assigned to a hit can be interpreted as meaning that in a database of the current size one might expect to see one match with a similar score simply by chance. An E value of zero means that one would not expect to see any matches with a similar score simply by chance. Occasionally, a string of X's or N's will result from a BLAST search. This is a result of automatic filtering of the query for low-complexity sequence that is performed to prevent artifactual hits. The filter substitutes any low-complexity sequence that it finds with the letter "N" in nucleotide sequence (*e.g.*, "NNNNNNNNNNNN") or the letter "X" in protein sequences (*e.g.*, "XXXXXXXXX"). Low-complexity regions can result in high scores that reflect compositional bias rather than significant position-by-position alignment. Wootton and Federhen, Methods Enzymol 266:554-571, 1996. Other BLAST results include sequences from the Patp database, which is a proprietary database that contains sequences published in patents and patent publications.

Please replace the paragraph on page 16, lines 1-13 with the following amended paragraph:

Tables 1G and 1H list the domain description from DOMAIN analysis results against NOV1. This indicates that the NOV1 sequence has properties similar to those of

other proteins known to contain these domains. The presence of identifiable domains in NOV1, as well as all other NOVX proteins, was determined by searches using software algorithms such as PROSITE, DOMAIN, Blocks, Pfam, ProDomain, and Prints, and then determining the Interpro number by crossing the domain match (or numbers) using the Interpro website. DOMAIN results may be collected from the Conserved Domain Database (CDD) with Reverse Position Specific BLAST analyses. This BLAST analysis software samples domains found in the Smart and Pfam collections. Sequences may also be analyzed according to a hmmpfam search against the HMM database (HMMER 2.1.1 (Dec 1998), Copyright (C) 1992-1998 Washington University School of Medicine). HMMER is freely distributed under the GNU General Public License.

Please replace the paragraph bridging pages 339-40 with the following amended paragraph:

The cell-free assays of the invention are amenable to use of both the soluble form or the membrane-bound form of NOVX protein. In the case of cell-free assays comprising the membrane-bound form of NOVX protein, it may be desirable to utilize a solubilizing agent such that the membrane-bound form of NOVX protein is maintained in solution. Examples of such solubilizing agents include non-ionic detergents such as n-octylglucoside, n-dodecylglucoside, n-dodecylmaltoside, octanoyl-N-methylglucamide, decanoyl-N-methylglucamide, Triton® X-100 (polyoxyethylene), Triton® X-114 (octylphenolpoly(ethyleneglycolether)$_n$ n=7 $^{-8}$ Thesit® (polyoxyethylene(9) lauryl alcohol), Isotridecypoly(ethylene glycol ether)$_n$, N-dodecyl--N,N-dimethyl-3-ammonio-1-propane sulfonate, 3-(3-cholamidopropyl) dimethylamminiol-1-propane sulfonate (CHAPS), or 3-(3-cholamidopropyl)dimethylamminiol-2-hydroxy-1-propane sulfonate (CHAPSO).